

Amendments to claims:

Claim 1. (Currently amended) A method of identifying a plant disease-resistance gene comprising:

- (a) providing a plant tissue sample comprising a mutant disease-resistance gene;
- (b) introducing by biolistic transformation into said plant tissue sample a candidate plant disease-resistance gene;
- (c) expressing said candidate plant disease-resistance gene within said plant tissue sample; and
- (d) determining whether said plant tissue sample exhibits a disease-resistance response, whereby a response identifies a plant disease-resistance gene.

Claim 2. (Currently amended) ~~A method~~ The method of claim 1, wherein said plant tissue sample comprises leaf, root, flower, fruit, or stem tissue.

Claim 3. (Original) The method of claim 1, wherein said candidate plant disease-resistance gene is obtained from a cDNA expression library.

Claim 4. (Original) The method of claim 1, wherein said disease-resistance response is the hypersensitive response.

Claim 5. (New) The method of claim 2, wherein said plant tissue sample comprises leaf tissue.

Claim 6. (New) The method of claim 1, wherein said plant tissue sample is infiltrated with a phytopathogenic bacterium.

Claim 7. (New) The method of claim 5, wherein said leaf tissue comprises a leaf, wherein one side of said leaf is infected with a phytopathogenic bacterium, and wherein the other side of said leaf is a noninfected control.

Claim 8. (New) The method of claim 1, wherein said candidate plant disease-resistance gene is co-introduced by biolistics with a reporter gene.

Claim 9. (New) The method of claim 8, wherein expression of said reporter gene serves as an indicator for the viability of the transformed cells of said plant tissue sample.

Claim 10. (New) The method of claim 8, wherein said candidate plant disease-resistance gene and said reporter gene are both expressed under the control of a constitutive promoter.

Claim 11. (New) The method of claim 6, wherein said phytopathogenic bacterium is *Pseudomonas syringae*.

Claim 12. (New) The method of claim 8, wherein said reporter gene is the *Escherichia coli uidA* gene encoding  $\beta$ -glucuronidase (GUS).

Claim 13. (New) The method of claim 10, wherein said constitutive promoter is the 35S promoter from Cauliflower mosaic virus.

Claim 14. (New) The method of claim 12, wherein differences in GUS activity are detected histochemically.

Claim 15. (New) The method of claim 11, wherein said phytopathogenic bacterium is *P. syringae* pv. *phaseolicola* 3121 (Psp 3121).